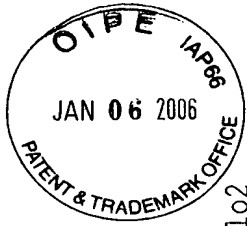




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1 M-----ARAKLPRSPSE-----GKAGPGGA-----PAGAAAPEE hSlo2
1 M-----ARAKLPRSPSE-----GKAGPGDT-----PAGSAAPEERSLACK
1 AREEGGSHSLPRVGSLLPGRMPLPDGARTPGGVCREARGGYTNRTFFDDGCCAPRRKIAA1422
30 P-HGLSPLLPARG--GGSVGS DV--GQRLPVEDEFSLDSSLSQ--VQVEFYVNENTFK hSlo2
30 P-HGLSPLLPTRG--GGSVGS DV--GQRLHVEDFSLDSSLSQ--VQVEFYVNENTFK rSLACK
61 PCAGD GALLDTAGFKMSDLDSEVLPLPPRYRFRDLLLGDPSFQND D R VQVEFYVNENTFKKIAA1422
80 ERLKLF FIKNQRSSLRIRLNFSLKLLTCLLYIVRVLLDDPALGIGCWGCPKQNYSFNDS hSlo2
80 ERLKLF FIKNQRSSLRIRLNFSLKLLTCLLYIVRVLLDDPDQIGICWGCTKYN YTFNGS rSLACK
121 ERLKLF FIKNQRSSLRIRLNFSLKLLTCLLYIVRVLLDDPALGIGCWGCPKQNYSFNDS KIAA1422
140 SSEINWAPI LWVERKMTLWAIQVIVAIISPLETMLLIYLSYKGNIEWEQIFRVSEFVLEMIN hSlo2
140 SSEFHWAPI LWVERKMTLWAIQVIVATISFLETMLLIYLSYKGNIEWEQIFHVSFVLEMIN rSLACK
181 SSEINWAPI LWVERKMTLWAIQVIVAIISFLETMLLIYLSYKGNIEWEQIFRVSEFVLEMIN KIAA1422
200 TLPFIIITIFWPPPLRNLFIPVFLNCWLAKHALENMINDFHRAILRTQSAMENQVLIILFCTLL hSlo2
200 TLPFIIITVFWPPPLRNLFIPVFLNCWLAKHALENMINDFHRAILRTQSAMENQVLIILFCTLL rSLACK
241 TLPFIIITIFWPPPLRNLFIPVFLNCWLAKHALENMINDFHRAILRTQSAMENQVLIILFCTLL KIAA1422
260 LCLVFTGTCGIIQHIERAGENLSLLTSEFYFCIVTFTSTVG YGDVTPK IWP S QLLV VIMICVA hSlo2
260 LCLVFTGTCGIIQHIERAGCNLNLTLTSEFYFCIVTFTSTVG FGDVTPK IWP S QLLV VILICVT rSLACK
301 LCLVFTGTCGIIQHIERAGENLSLLTSEFYFCIVTFTSTVG YGDVTPK IWP S QLLV VIMICVA KIAA1422
320 LVVLP LQFEEELVYLWMERQKSGGNYSRHRAQTEKHVVL CVSSLKIDLLMDFLN E F YAHPR hSlo2
320 LVVLP LQFEEELVYLWMERQKSGGNYSRHRAQTEKHVVL CVSSLKIDLLMDFLN E F YAHPR rSLACK
361 LVVLP LQFEEELVYLWMERQKSGGNYSRHRAQTEKHVVL CVSSLKIDLLMDFLN E F YAHPR KIAA1422
380 LQDY YV VILCPT EMDVQVRRVLQIPLWSQRVIY LQGSAL KDQDLMRAKMDNGEACFILSS hSlo2
380 LQDY YV VILCPT EMDVQVRRVLQIPLWSQRVIY LQGSAL KDQDLMRAKMDNGEACFILSS rSLACK
421 LQDY YV VILCPT EMDVQVRRVLQIPLWSQRVIY LQGSAL KDQDLMRAKMDNGEACFILSS KIAA1422
440 RNEVDRTAADHQTI LRAWAVKDFAPNCPLYVQI LKPKENKFHVKFADHVVC E ECKYAML A hSlo2
440 RNEVDRTAADHQTI LRAWAVKDFAPNCPLYVQI LKPKENKFHVKFADHVVC E ECKYAML A rSLACK
481 RNEVDRTAADHQTI LRAWAVKDFAPNCPLYVQI LKPKENKFHVKFADHVVC E ECKYAML A KIAA1422

FIG. 1



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500 LNCICPATSTLITLLVHTSRGQEGQESPEQWQRMYGRCSGNEVYHIRMGDSKFFREYEGK hSlo2
500 LNCICPATSTLITLLVHTSRGQEGQESPEQWQRMYGRCSGNEVYHIRMGDSKFFREYEGK rSLACK
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560 SFTYAAFHAHKKYGVCLIGLKREDNKSILLNPGPRHILAAASDTCFYINITKEENS AFI F K hSlo2
560 SFTYAAFHAHKKYGVCLIGLKREDNKSILLNPGPRHILAAASDTCFYINITKEENS AFI F K rSLACK
601 SFTYAAFHAHKKYGVCLIGLKREDNKSILLNPGPRHILAAASDTCFYINITKEENS AFI F K KIAA1422

620 QEEKRKKRAFSGQGLHEGPARLPVHSIIASM--VAMD LQGT EHRPTQSGGGGGGSKLALP hSlo2
620 QEEKQNRRLAGQALYEGPSRLPVHSIIASM--VAMD LQNTDCRPSQGGSGGGGKLTLP rSLACK
661 QEEKRKKRAFSGQGLHEGPARLPVHSIIASMGTVAMD LQGT EHRPTQSGGGGGGSKLALP KIAA1422

678 TENGSGSRRRPSIAPVLELADSSALLPCDLLSDQSEDEVTPSDDEGLSVVEYVKGYPPNSP hSlo2
678 TENGSGSRRRPSIAPVLELADSSALLPCDLLSDQSEDEVTPSDDEGLSVVEYVKGYPPNSP rSLACK
722 TENGSGSRRRPSIAPVLELADSSALLPCDLLSDQSEDEVTPSDDEGLSVVEYVKGYPPNSP KIAA1422

738 YIVSSPTLCHLLPVKAPFCCCLRLDKGCKKHNSYEDAKAYGEFKNKLIIVSAETAGNGLYNFI hSlo2
738 YIGSSPTLCHLLPVKAPFCCCLRLDKGCKKHNSYEDAKAYGEFKNKLIIVSAETAGNGLYNFI rSLACK
781 YIGSSPTLCHLLPVKAPFCCCLRLDKGCKKHNSYEDAKAYGEFKNKLIIVSAETAGNGLYNFI KIAA1422

798 VPLRAYYRSRKEINPIVLLLDNKKPDHFFLEAICCFPMVYYMEGSVDNLDSSLQCCGIIYAD hSlo2
798 VPLRAYYRSRKEINPIVLLLDNKKPDHFFLEAICCFPMVYYMEGSVDNLDSSLQCCGIIYAD rSLACK
841 VPLRAYYRSRKEINPIVLLLDNKKPDHFFLEAICCFPMVYYMEGSVDNLDSSLQCCGIIYAD KIAA1422

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901 NLVVVDKESTMSAEEDYMADAKTIIVNVQTMFRLLFPSSLITTELTHPSNMRRFMQFRAKDSY KIAA1422

918 SLALSKLEKRENGSNLAFMFRLPFAAGRVSISMLDITLLYQSFVKDYMITITRLLGL hSlo2
918 SLALSKLEKRENGSNLAFMFRLPFAAGRVSISMLDITLLYQSFVKDYMITITRLLGL rSLACK
961 SLALSKLEKRENGSNLAFMFRLPFAAGRVSISMLDITLLYQSFVKDYMITITRLLGL KIAA1422

978 DTPGSGGYLCAMKITEGDLWIRTYGRRLFQKLCSSSAEIPIGIYRTESHVFTSEPHDLRA hSlo2
978 DTPGSGGYLCAMKVTEGDLWIRTYGRRLFQKLCSSSAEIPIGIYRTECHVFS-SEPHDLRA rSLACK
1021 DTPGSGGYLCAMKITEGDLWIRTYGRRLFQKLCSSSAEIPIGIYRTESHVFTSEPHDLRA KIAA1422

FIG. 1 (CONT.)



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1038QSQISVNVEDCEDTREVKGPGWSRAGTGGSS-QGRHTGGGDPAEHPLLRRKSLQWARRLS hSlo2
1037QSQISVNVEDCEDTREVKGPGWGTAAAGGSGTHGRHGGSADPVEHPLLRRKSLQWARRLS rSLACK
1081QSQISVNVEDCEDTREVKGPGWSRAGTGGSS-QGRHTGGGDPAEHPLLRRKSLQWARRLS KIAA1422

1097RKAPKQAGRAA-AAEWISQQRSLSYRRSERQELSELVKNRMKHGLGLPTTGYEDVANLTAS hSlo2
1097RKSSKQAGKAPMTTDWITQQRLSLYRRSERQELSELVKNRMKHGLGLPTTGYEDVANLTAS rSLACK
1140RKAPKQAGRAA-A

1156DVMNRVNLGYLQDEMNDH-QNTLSYVLIINPPPDTRLEPSDIVYLIRSDPLAHVASSSQSR hSlo2
1157DVMNRVNLGYLQDEMNDHHQNTLSYVLIINPPPDTRLEPNDIVYLIRSDPLAHVTSSSQSR rSLACK
KIAA1422

1215KSSCASHKLSSCNPETRDETQL hSlo2
1217KSSCSNKLSSCNPETRDETQL rSLACK
KIAA1422

FIG. 1 (CONT.)



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```

1  MV-----DLESEVPPPPRYRFRDLLLL--GDQGWQNDDR-----S1o4
1  MARAKLPRSPSEKAGPGAGAAPEEPH-GLSPLLPARGGSGVDGQRLPVEDFS S1o2
333 -----VQVEFYMNENTFERLKLFFIKNQRSSLRIRLENPSLKLSCLLYIIRVLLLEN S1o4
60  LDSSLQVQVEFYVNENTFERLKLFFIKNQRSSLRIRLENPSLKLTLCLLYIVRVLLDD S1o2
86  PSQGN-----EWSHIFVWNRSPLPLWGLQVSVVALISLFFETILLGYLS S1o4
120 PALGIGCWGCPKQYSFNDSSSEINWAPILMVERKMTLWAIQVIVAIIISFLETMLLIYLS S1o2
127 YKGNIEWEQILRIPFILLEIINAVPFIISFWPSLRNLFVPVFLNCWLAKHALENMINDLHR S1o4
180 YKGNIEWEQIFRVSRLVLEMINTLPEIITIFWPPLRNLFIPVFLNCWLAKHALENMINDFHR S1o2
187 AIQRTQSAMFNQVLILISTLLCLIFTICIGIQHLEIGKKLNLFDSLFCIVTFSTVGFG S1o4
240 AI LRTQSAMFNQVLILFCTLLCLVFTGTCGIIQHLELAGENLSLTSFYFCIVTFSTVGYG S1o2
247 DVTPETWSSKLFVAMICVALVLP IQFEQLAYLWMERQKSGGNYSRHRAQTEKHVVLCV S1o4
300 DVTPKIWPSQLLVIMICVALVLP LQFEELVYLWMERQKSGGNYSRHRAQTEKHVVLCV S1o2
306 SSLKIDLLMDFLNEFYAHPRLQDYVVLCPTEM DVVRRVLQIPMWSQRVIY LQGSALK S1o4
3360 SSLKIDLLMDFLNEFYAHPRLQDYVVLCPTEM DVVRRVLQIP LWSQRVIY LQGSALK S1o2
367 DQDL LRAKMDDAEACFILSSRCEVDRTSSDHQ TILRAWAVKDFAPNCPLYVQILKPENKF S1o4
420 DQDL MRAKMDNGEACFILSSRNEVDRTAADHQ TILRAWAVKDFAPNCPLYVQILKPENKF S1o2
427 HIKFADHVVCEEEFKYAMLALNCICPATSTLITLLVHTSRGQEGQQSPEQWQKMYGRCSG S1o4
460 HVKFADHVVCEEECKYAMLALNCICPATSTLITLLVHTSRGQEGQESPEQWQRMYGRCSG S1o2
487 NEVYHIVLEESTFFAEYEGKSFTYASFHAHKKFGVCLLIGVRRREDNKNILLNPGPRYIMNS S1o4
540 NEVYHIRMGD SKFFREYEGKSFTYAAFHAHKKYGVCLLIGLKREDNKSILLNPGPRHILAA S1o2
547 TDICFYINITKEENSAF--KNQDQQRKSNVS-RSFYHGCP SRLPVHSIIASMGTV AIDLQD S1o4
600 SDTCFYINITKEENSAFIFKQEEKRKKRAFSGQGLHEGPARLPVHSIIASM-VAMD LQG S1o2

```

FIG. 2



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604 TSCRSA-----SGPTLSLPTEGSKEIRRRPSIAPVLEVADTSSIQTCDLLSDQSEDETP S104
658 TEHRPTQSGGGGGSKLALPTENGSGSRRRPSIAPVLELADSSALLPCDLLSDQSEDEVTP S102

658 -DEEMSSNLEYAKGYPPYSPYIGSSPTFCHLLHEKVFPCCRLRLDKSCQHNYVEDAKAYGF S104
718 SDEGLSVVEYVKGYPNPSYIVSSPTLCHLLPVKAPFCCLRLDKGCKHNSYEDAKAYGF S102

717 KNKLIIVAAETAGNGLYNFIVPLRAYRPPKELNPIVLLLDNPPDMHFLDAICWFPMVYY S104
778 KNKLIIVSAETAGNGLYNFIVPLRAYRSRKELNPIVLLLDNKPDDHFLDAICCFPMVYY S102

777 MVGSIIDNLDLLRCGVTFANMVVDKESTMSAEDYMADAKTIIVNVQTLFRFSSLSII S104
838 MEGSVDNLDLSLLCGIYADNLVVVDKESTMSAEDYMADAKTIIVNVQTMERLFP S102

837 TELTHPANMRFMQFRAKDCYSLALSKEKKERERGSNLA FMERLPFAAGRVFSISM LDTL S104
898 TELTHPSNMRFMQFRAKDSYSLALSKEKKERERENGSGNLA FMERLPFAAGRVFSISM LDTL S102

897 LYQSFVKDYMITITRLLGLDTPD SGFLCSMKITADDLWIRTYARLYQKLCSS TGDVPI S104
958 LYQSFVKDYMITITRLLGLDTPD SGYLCAMKITEGDLWIRTYGR LFQKLCSSSAE IPI S102

957 GIYRTESQKLTSE-----SQISISVEEWEDTKDSKEQGHHR-----SNHRNSTSSD S104
1018 GIYRTESHVFTSEPHDLRAQSQISVNVEDCEDTREVKGPWGSRAGTGGSSQGRHTGGGD S102

1004 QSDHPLLRKSMQWARRLSRKGPKHSGKTA--EKITQQRLNLYRRS ERQELAE LVKNRMK S104
1078 PAEHPLLRKSLQWARRLSRKAPKQAGRAAAAEWISQQRLSLYRRS ERQELSELVKNRMK S102

1062 HGLGSTVGY-----DEMNDHQSTLSYILINPSPDTRIELNDVVY S104
1138 HGLPTTGYEDVANLTASDV MNRVNLGYLQDEMNDHQNTLSYVLINPPDTRLEPSD IY S102

1101 LIRPDPLAYLPNSEPSRRNSICNVT-----GQDSREETQL.
1198 LIRSDPLAHAVASSQSRKSS-CSHKLSSCNPETRDETQL.
S104
S102

FIG. 2 (CONT.)



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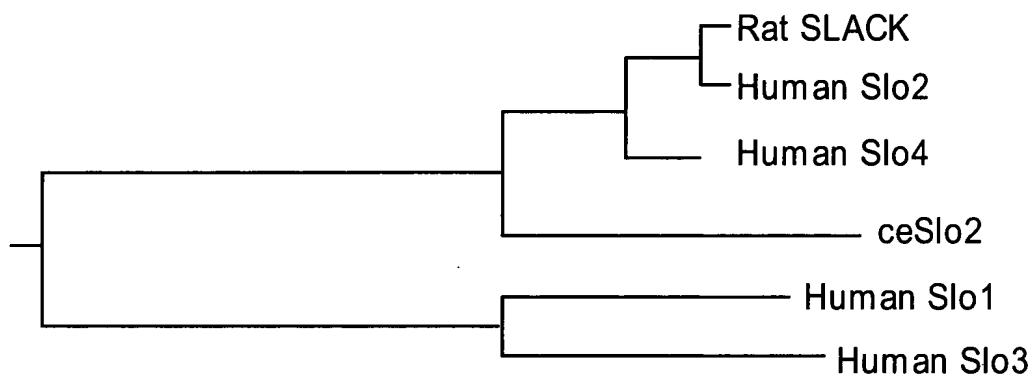


FIG. 3



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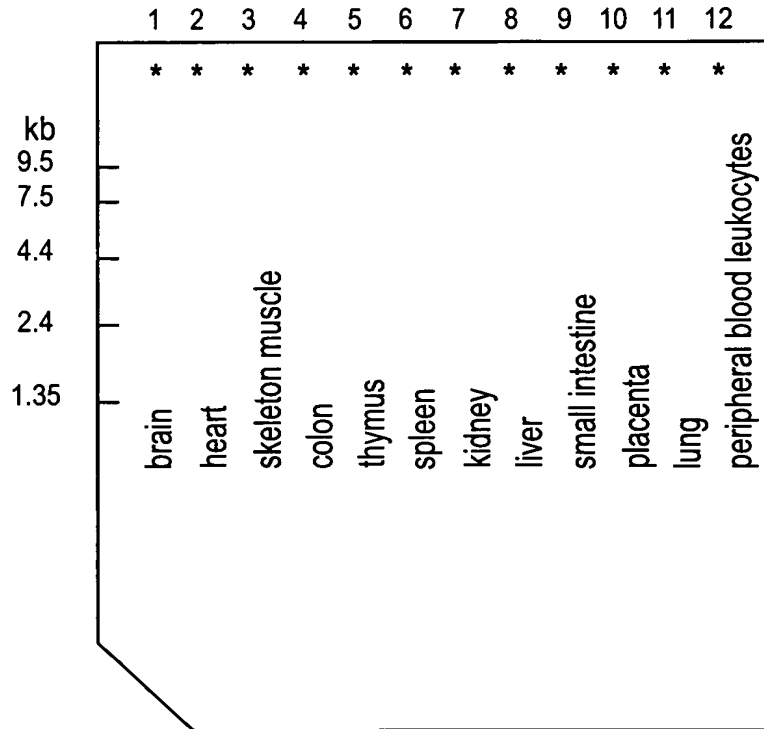


FIG. 4A



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	1	2	3	4	5	6	7	8
A	whole brain	amygdala	caudate nucleus	cerebellum	cerebral cortex	frontal lobe	hippocampus	medulla oblongata
B	occipital lobe	putamen	substantia nigra	temporal lobe	thalamus	nucleus accumbens	spinal cord	
C	heart	aorta	skeletal muscle	colon	bladder	uterus	prostate	stomach
D	testis	ovary	pancreas	pituitary gland	adrenal gland	thyroid gland	salivary gland	mammary gland
E	kidney	liver	small intestine	spleen	thymus	peripheral leukocyte	lymph node	bone marrow
F	appendix	lung	trachea	placenta				
G	fetal brain	fetal heart	fetal kidney	fetal liver	fetal spleen	fetal thymus	fetal lung	
H	yeast total RNA 100 mg	yeast tRNA 100 mg	E. coli rRNA 100 mg	E. coli DNA 100 mg	poly r(A) 100 mg	human Cot ¹ DNA 100 mg	human DNA 100 mg	human DNA 500 mg
	1	2	3	4	5	6	7	8

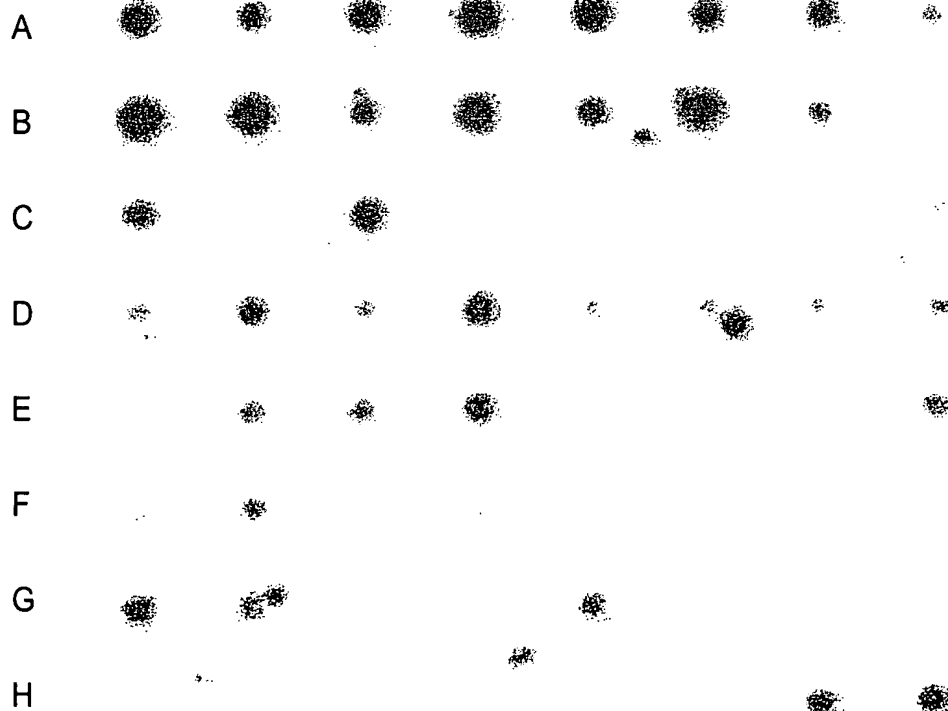


FIG. 4B



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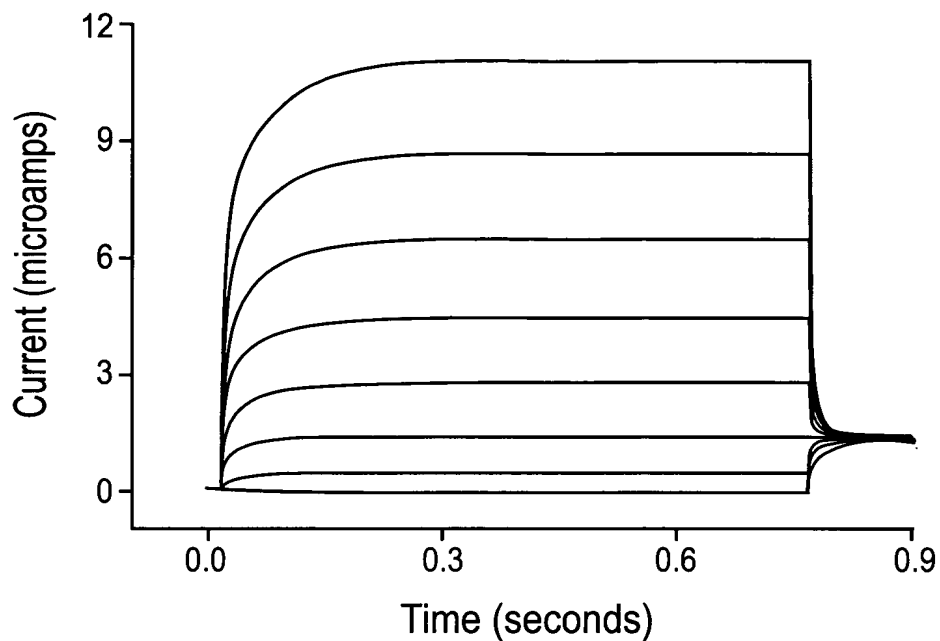


FIG. 5A

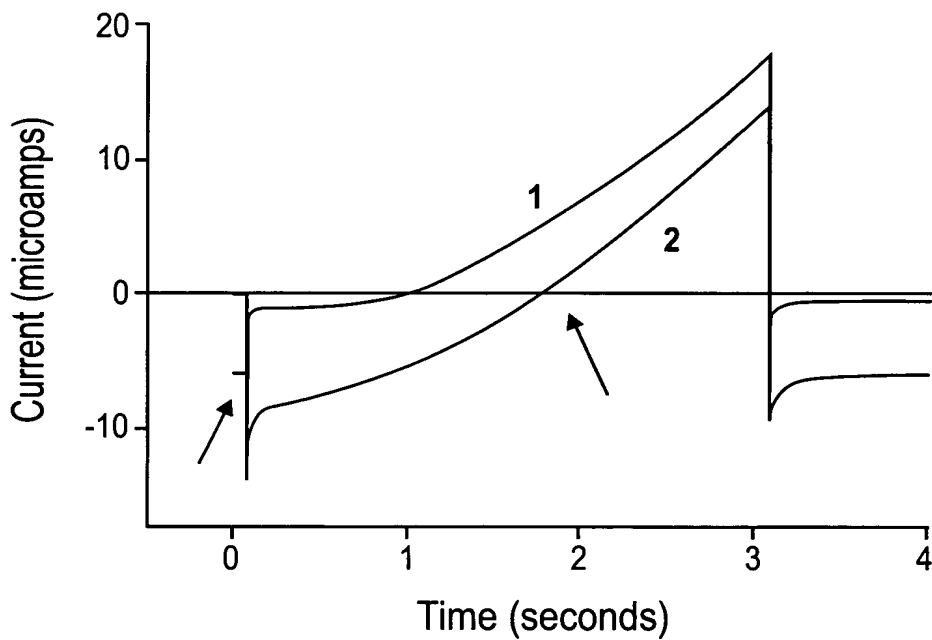


FIG. 5B



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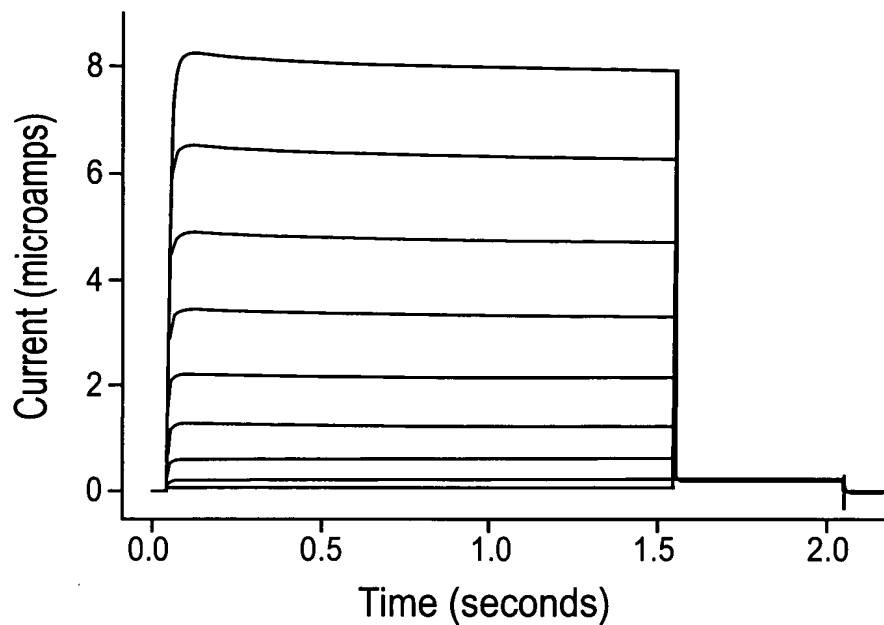


FIG. 6A

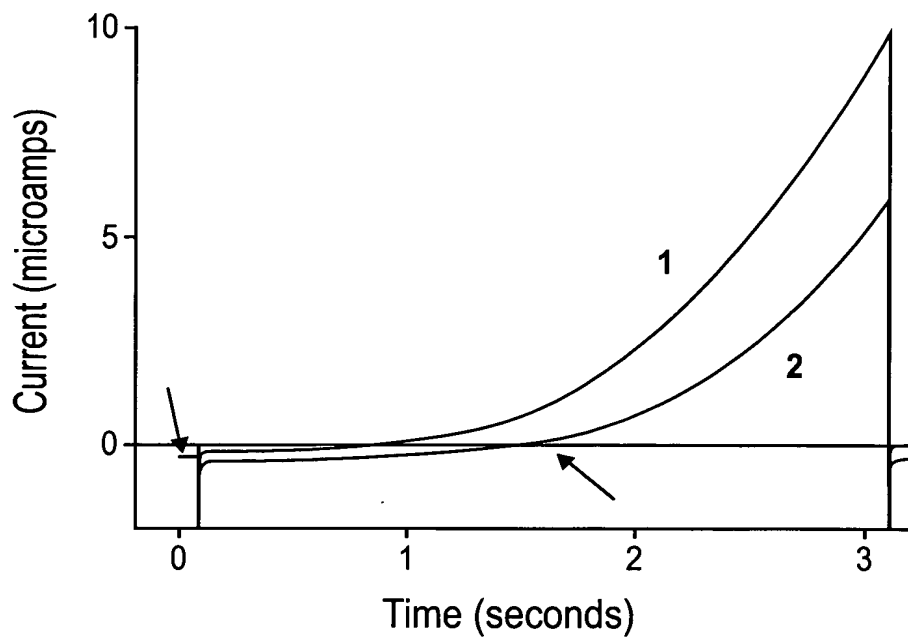


FIG. 6B



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Slo4 Northern Blot

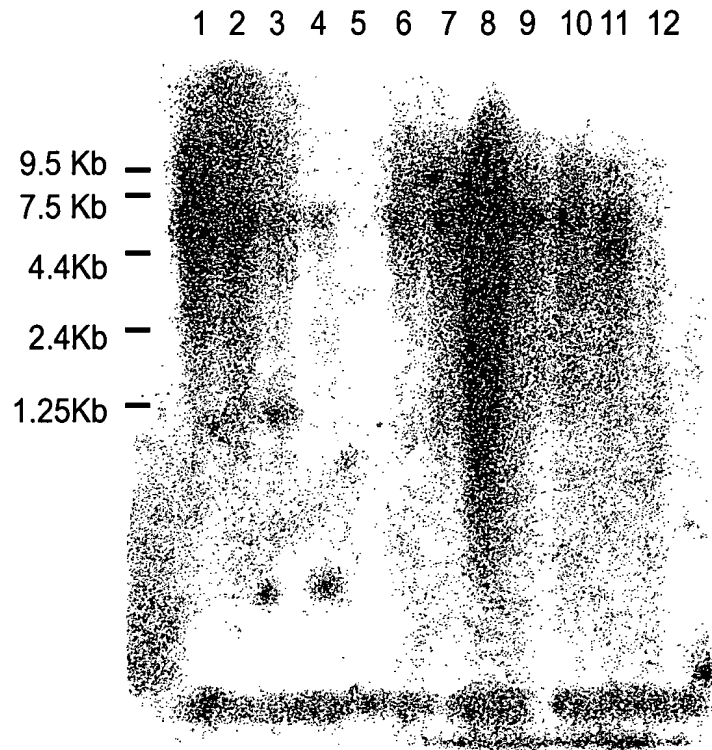


FIG. 7A



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Slo4 mRNA Dot Blot

	1	2	3	4	5	6	7	8	9	10	11	12
A	whole brain	cerebellum, left	substantia nigra	heart	esophagus	colon, transverse	kidney	lung	liver	leukemia, HL-60	fetal brain	yeast total RNA
B	cerebral cortex	cerebellum, right	nucleus accumbens	aorta	stomach	colon, descending	skeletal muscle	placenta	pancreas	Hela	fetal heart	yeast tRNA
C	frontal lobe	corpus callosum	thalamus	atrium, left	duodenum	rectum	spleen	bladder	adrenal gland	leukemia, K-562	fetal kidney	E. coli tRNA
D	parietal lobe	amygdala	pituitary gland	atrium, right	jejunum		thymus	uterus	thyroid gland	leukemia, MOLT-4	fetal liver	E. coli DNA
E	occipital lobe	caudate nucleus	spinal cord	ventricle, left	ileum		peripheral blood leukocyte	prostate	salivary gland	Burkitt's lymphoma, Raji	fetal spleen	poly r(A)
F	temporal lobe	hippo-campus		ventricle, right	ileocecum		lymph node	testis	mammary gland	Burkitt's lymphoma, Daudi	fetal thymus	human C ₀ t-1 DNA
G	p. g. * of cerebral cortex	medulla oblongata		inter-ventricular septum	appendix		bone marrow	ovary		colorectal adeno-carcinoma, SW480	fetal lung	human DNA 100 mg
H	pons	putamen		apex of the heart	colon, ascending		trachea			lung carcinoma, A549		human DNA 500 mg

* paracontral gyrus

FIG. 7B



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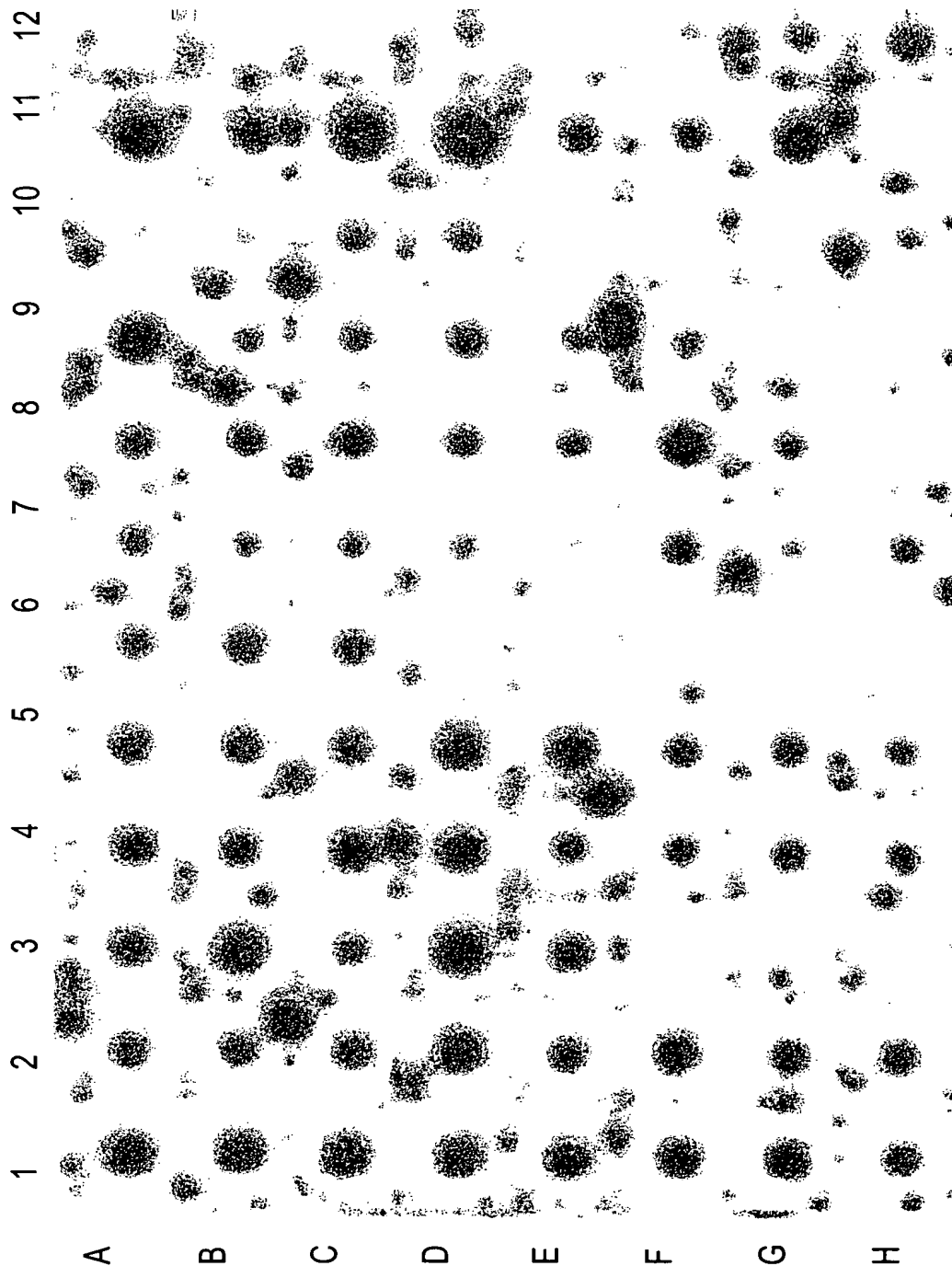


FIG. 7B (CONT.)